

	(1)	1	10	20	30	40	50	60	70
gi_3228664_gb_AAC39136.1_	(1)	-	-	-	-	-	-	-	-
gi_3228670_gb_AAC39137.1_	(1)	-	-	-	-	-	-	-	-
gi_3228666_gb_AAC39907.1_	(1)	MLGFI	TRPPH	FLSL	LLCPGLR	IPQLSVL	CAQPRPR	AMAISSS	SC
gi_3228668_gb_AAC40185.1_	(1)	MLGFI	TRPPH	-	-	QLLCT	GYRLLR	TPVLCTQ	PRPRTMSSSTS
gi_3242980_gb_AAC40184.1_	(1)	MLGFI	TRPPH	-	-	QLLCT	GYRLLR	IPVLCTQ	PRPRTMSSSTS
gi_2294001_emb_CAA02248.1_	(1)	-	-	-	-	-	-	-	-
gi_216934_dbj_BAA01994.1_	(1)	-	-	-	-	-	-	-	-
gi_508735_gb_AAA19627.1_	(1)	-	-	-	-	-	-	-	-
gi_508733_gb_AAB60275.1_	(1)	-	-	-	-	-	-	-	-
gi_1469912_gb_AAB05220.1_	(1)	-	-	-	-	-	-	-	-
gi_1389699_gb_AAB05221.1_	(1)	-	-	-	-	-	-	-	-
gi_1181615_dbj_BAA11770.1_	(1)	-	-	-	-	-	-	-	-
gi_1171482_dbj_BAA09645.1_	(1)	-	-	-	-	-	-	-	-
gi_5953961_gb_AAE06465.1_	(1)	-	-	-	-	-	-	-	-
SEQIDNO:2-09751299		-	-	-	-	-	-	-	-
SEQIDNO:4-09751299		-	-	-	-	-	-	-	-
Consensus	(1)	-	-	-	-	-	-	-	-

	71	80	90	100	110	120	130	140
gi_3228664_gb_AAC39136.1	I E A G E K K C E M V F L P E C F D F I G L - - - - -	N K N E Q I D L A M A T D C E Y M E K Y R E L A R K H N T						
gi_3228670_gb_AAC39137.1	V D R A K S Q N A C M L F L P E C C D F V G E - - - - -	S R T Q T I E L S E G L D G E L M A Q Y R E L A K C N K I						
gi_3228666_gb_AAC39907.1	V R E A R L G A C L A F L P E A F D F I A R - - - - -	D P A E T L H L S E P L G G K L L E E Y T Q L A R E C G L						
gi_3228668_gb_AAC40185.1	V Q E A R L G A C L A F L P E A F D F I A R - - - - -	N P A E T L L L S E P L N G D L L G Q Y S Q L A R E C G I						
gi_3242980_gb_AAC40184.1	V Q E A R L G A C L A F L P E A F D F I A R - - - - -	N P A E T L L L S E P L N G D L L G Q Y S Q L A R E C G I						
gi_2294001_emb_CAA02248.1	I A E A S M G A K V I G T P E A F I P G Y P - - - - -	Y W I W T S N - M D F T G M M W A V L F K N A I E I P S K E V Q Q I S D A A K K N G V						
gi_216934_dbj_BAA01994.1	I A E A R N G C E L V A F P E V F I P G Y P - - - - -	Y H I W D S P L A G M A K F A V R Y H E N S L T M D S P H V Q R L L D A A R D H N I						
gi_508735_gb_AAA19627.1	I V E A S K G A K L V L F P E A F I G G Y P R G F R F G L A V G V H N E E G R D E F R N Y H A S A I K V P G P E V E R L A E L A G K N N V							
gi_508733_gb_AAB60275.1	I V E A S K G S E L V V F P E A F I G G Y P R G F R F G L G V G V H N E E G R D E F R K Y H A S A I K V P G P E V E K L A E L A G K N N V							
gi_1469912_gb_AAB05220.1	I V E A A T K G S E L V V F P E A F I G G Y P R G F R F G L G V G V H N E E G R D E F R K Y H A S A I K V P G P E V E K L A E L A G K N N V							
gi_1389699_gb_AAB05221.1	I V E A A S K G A E L V L F P E P E G F I G G Y P R G F R F G L A V G V H N E E G R D E F R K Y H A S A I H V P G P E V A R L A D V A R K N H V							
gi_1181615_dbj_BAA11770.1	L A E A S Y G A Q L V V F P E A F I G G Y P R G S T F G V S I G N R T A K G K E E F R K Y H A S A I D V P G P E V D R L A A M A G K Y K V							
gi_1171482_dbj_BAA09645.1	L A E A S Y G A Q L V V F P E A F I G G Y P R G S T F G V S I G N R T A K G K E E F R K Y H A S A I D V P G P E V D R L A A M A G K Y K V							
gi_5953961_gb_AAE06465.1	V E E A S R A G A D L I A F P E T W I P G Y P - - - - -	W F L W L D S - V A W Q S Q Y F I R Y P Q N S L D L D G S E F A A I R E A A R K N D I						
SEQIDNO:2-09751299	I E Q A A K Q D V R L I A F P E T W I P G Y P - - - - -	F W I W L G A - P A W G M R F V Q R Y F F E N S L V R G S K Q W Q A L A D A A R R H G M						
SEQIDNO:4-09751299	M E A A R N N A R L I A F P E T W I P G Y P - - - - -	W F L W L D S - P A W A M Q F V R Q Y H E N S L E L D G P Q A K R I S D A A K R L G I						
Consensus	I E A A S G A L V F P E A F I G Y P . . . F L V	F K Y H A I L G P E V R L A E L A R K I						

Section 3

	141	150	160	170	180	190	200	210
gi_3228664_gb_AAC39136.1_	(141)	WLSLGGIHHKDPDSD--AAHPWNT	HLT	IDSDGVTRAE	YNK	LHLFDLE	IPGKVR	LMESFSKAGTEM
gi_3228670_gb_AAC39137.1_	(91)	WISLGGVHERN----	DQKIFNAHV	LNEKGE	LA	AVYRK	THMFDV	TK-EVRLRES
gi_3228666_gb_AAC39907.1_	(109)	WLSLGGFHERG	QDWEQTK	YNCHV	LNSKGA	VVA	TYRKT	HLCDVE
gi_3228668_gb_AAC40185.1_	(123)	WLSLGGFHERG	QDWEQNK	YNCHV	LNSKGS	VVA	TYRKT	HLCDVE
gi_3228668_gb_AAC40185.1_	(119)	WLSLGGFHERG	QDWEQNK	YNCHV	LNSKGS	VVA	TYRKT	HLCDVE
gi_3242980_gb_AAC40184.1_	(119)	WLSLGGFHERG	QDWEQNK	YNCHV	LNSKGS	VVA	TYRKT	HLCDVE
gi_2294001_emb_CAA02248.1_	(97)	YVCMVSEKDN----	ASLYLTQLW	FDPP	GNLIGK	HRK	FKPT	SSERA
gi_216934_dbj_BAA01994.1_	(99)	AVVVGISERD	-----	GSLYMTQLV	IDADGQ	LVAR	RK	KLKPT
gi_508735_gb_AAA19627.1_	(120)	HLVMGAIIEKDG	-----	YTLYCTAL	FFSPQ	QGF	LGGK	HRK
gi_508733_gb_AAB60275.1_	(113)	YLVMGAIIEKDG	-----	YTLYCTAL	FFSPQ	QGF	LGGK	HRK
gi_1469912_gb_AAB05220.1_	(113)	YLVMGAIIEKDG	-----	YTLYCTAL	FFSPQ	QGF	LGGK	HRK
gi_1389699_gb_AAB05221.1_	(120)	YLVMGAIIEKDG	-----	YTLYCTAL	FFSPQ	QGF	LGGK	HRK
gi_1181615_dbj_BAA11770.1_	(124)	YLVMGVIERDG	-----	YTLYCTAL	FFDSQ	QGHY	LGGK	HRK
gi_1171482_dbj_BAA09645.1_	(124)	YLVMGVIERDG	-----	YTLYCTAL	FFDSQ	QGHY	LGGK	HRK
gi_5953961_gb_AAE06465.1_	(99)	AITMGFSEERGH	-----	GSLYMGQA	VI	IERDGV	VVR	TRR
SEQIDNO:2-09751299	(98)	HVMAGYSERAG	-----	GSLYMGQA	VI	IERDGV	VVR	TRR
SEQIDNO:4-09751299	(95)	MVTLGMSERVG	-----	GTLYISQW	F	IGDN	NGDT	IGAR
Consensus (141)		YLVMGGIERDG		TLY T LLF QG	LLGK	HRK	KL PT LER	IWG GDGS

Section 4

	211	220	230	240	250	260	270	280
gi_3228664_gb_AAC39136.1_	(211)	TPIGRLGLST	CTCYD	VRFF	PELSLWNRKR	GAQ	L	SFF
gi_3228670_gb_AAC39137.1_	(159)	TPVGGHGLQ	CTCYD	LRFAEP	AVL	RK	L	GAN
gi_3228666_gb_AAC39907.1_	(173)	TPAGKIGLAV	CYD	MRFF	PELSL	LA	QA	GA
gi_3228668_gb_AAC40185.1_	(189)	TPAGKVGLAI	CYD	MRFF	PELSL	LA	QA	GA
gi_3242980_gb_AAC40184.1_	(189)	TPAGKVGLAI	CYD	MRFF	PELSL	LA	QA	GA
gi_2294001_emb_CAA02248.1_	(153)	TEYGNELGLQ	CWEHAL	PL	NI	AM	GS	LN
gi_216934_dbj_BAA01994.1_	(155)	MEFARLGA	LNCWE	HFQ	TL	TKY	AM	YS
gi_508735_gb_AAA19627.1_	(176)	TPIGKIIGAAI	CWENR	MP	PE	YRT	AL	YAK
gi_508733_gb_AAB60275.1_	(169)	TPIGKLGAAI	CWENR	MP	PE	YRT	AL	YAK
gi_1469912_gb_AAB05220.1_	(169)	TPIGKLGAAI	CWENR	MP	PE	YRT	AL	YAK
gi_1389699_gb_AAB05221.1_	(176)	TPIGKLGAAI	CWENR	MP	PE	YRT	AL	YAK
gi_1181615_dbj_BAA11770.1_	(180)	TPLGKIGAAI	CWENR	MP	PE	YRT	AL	YAK
gi_1171482_dbj_BAA09645.1_	(180)	TPLGKIGAAI	CWENR	MP	PE	YRT	AL	YAK
gi_5953961_gb_AAE06465.1_	(155)	TSLGRVGS	LCCWE	HLQ	PL	TKY	AM	YS
SEQIDNO:2-09751299	(154)	TAIGRLGALCC	WEHI	Q	PL	SKY	AM	YS
SEQIDNO:4-09751299	(151)	TSVGRLLG	LCCWE	HLQ	PL	TKY	AL	YA
Consensus (211)		TPIGKLGAAICWE	R PL R	ALYA	G	EIY	APTA	

Section 5

	281	290	300	310	320	330	340	350
gi_3228664_gb_AAC39136.1_	(281)	LAHWE	TL	RARA	TE			
gi_3228670_gb_AAC39137.1_	(281)	LAHWE	TL	RARA	TE			
gi_3228666_gb_AAC39907.1_	(281)	LAHWE	TL	RARA	TE			
gi_3228668_gb_AAC40185.1_	(281)	LAHWE	TL	RARA	TE			
gi_3242980_gb_AAC40184.1_	(281)	LAHWE	TL	RARA	TE			
gi_2294001_emb_CAA02248.1_	(281)	LAHWE	TL	RARA	TE			
gi_216934_dbj_BAA01994.1_	(281)	LAHWE	TL	RARA	TE			
gi_508735_gb_AAA19627.1_	(281)	LAHWE	TL	RARA	TE			
gi_508733_gb_AAB60275.1_	(281)	LAHWE	TL	RARA	TE			
gi_1469912_gb_AAB05220.1_	(281)	LAHWE	TL	RARA	TE			
gi_1389699_gb_AAB05221.1_	(281)	LAHWE	TL	RARA	TE			
gi_1181615_dbj_BAA11770.1_	(281)	LAHWE	TL	RARA	TE			
gi_1171482_dbj_BAA09645.1_	(281)	LAHWE	TL	RARA	TE			
gi_5953961_gb_AAE06465.1_	(281)	LAHWE	TL	RARA	TE			
SEQIDNO:2-09751299	(281)	LAHWE	TL	RARA	TE			
SEQIDNO:4-09751299	(281)	LAHWE	TL	RARA	TE			
Consensus (281)		LAHWE	TL	RARA	TE			

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	(281)	281	290	300	310	320	330	340	350																																													
gi_3228664_gb_AAC39136.1_	(215)	NQCYVAA	QQTGAHN	-----	PK	--RQSY	GHS	MVVD	PWGA	VVAQC	SER--	VDMCFAE																																										
gi_3228670_gb_AAC39137.1_	(229)	TQCFVAA	QIGWHN	-----	QK	--RQSW	GHS	IVSP	WGN	VLA	DCSEQ	E-LDIGTAE																																										
gi_3228666_gb_AAC39907.1_	(249)	TQCYVAA	QCGRHH	-----	EK	--RAS	GHS	MVVD	PWGT	VVA	RCSEG	--PGICLAR																																										
gi_3228668_gb_AAC40185.1_	(245)	SQCYVIA	QCGRHH	-----	ET	--RAS	GHS	MVVD	PWGT	VVA	RCSEG	--PGICLAR																																										
gi_3242980_gb_AAC40184.1_	(245)	SQCYVIA	QCGRHH	-----	ET	--RAS	GHS	MVVD	PWGT	VVA	RCSEG	--PGICLAR																																										
gi_2294001_emb_CAA02248.1_	(223)	NQYVIM	STNLVG	-----	QD	MID	MIG	KDEF	SKNF	PLG	SGNT	AIISNT	GEILAS	IPQDA	EGIAVAE																																							
gi_216934_dbj_BAA01994.1_	(218)	GQTFVCT	QVVT	-----	PE	AHE	FFC	DND	EQ	RKL	I	GRGG	FARI	I	CPD	GRDLAT	PLADE	EGILYAD																																				
gi_508735_gb_AAA19627.1_	(228)	GQCFVLS	AHQF	CKRREF	EPDYL	LFND	I	VD	TK	E	H	PT	VS	GGG	--	S	V	I	S	P	L	G	K	V	L	A	G	P	N	Y	E	S	--	E	G	L	V	T	A	D														
gi_508733_gb_AAB60275.1_	(221)	GQCFVLS	ACQF	CLRKDF	PDYLF	FTD	WY	LF	TD	WY	DK	EP	DS	I	V	S	Q	GG	--	S	V	I	S	P	L	G	K	V	L	A	G	P	N	F	E	S	--	E	G	L	I	T	A	D										
gi_1469912_gb_AAB05220.1_	(221)	GQCFVLS	ACQF	CLRKDF	PDYLF	FTD	WY	LF	TD	WY	DK	EP	DS	I	V	S	Q	GG	--	S	V	I	S	P	L	G	K	V	L	A	G	P	N	F	E	S	--	E	G	L	I	T	A	D										
gi_1389699_gb_AAB05221.1_	(228)	GQCFVLS	ACQF	CRKHFP	PDYLF	FTD	WY	LF	TD	WY	DK	EP	DS	I	V	S	Q	GG	--	S	V	I	S	P	L	G	K	V	L	A	G	P	N	F	E	S	--	E	G	L	V	T	A	D										
gi_1181615_dbj_BAA11770.1_	(232)	GQCFVLS	ANQF	CRKDYPP	PPEYV	FSG	-	TE	DL	T	P	DS	I	V	C	A	G	G	--	S	V	I	S	P	S	G	A	V	L	A	G	P	N	Y	E	G	--	E	A	L	I	S	A	D										
gi_1171482_dbj_BAA09645.1_	(232)	GQCFVLS	ANQF	CRKDYPP	PPEYV	FSG	T	E	DL	T	P	DS	I	V	C	A	G	G	--	S	V	I	S	P	S	G	A	V	L	A	G	P	N	Y	E	G	--	E	A	L	I	S	A	D										
gi_5953961_gb_AAE06465.1_	(218)	GQTYVLA	P	CAVIG	-----	D	A	G	WE	A	F	A	D	T	E	K	R	Q	L	I	H	K	G	G	G	Y	A	R	I	Y	G	P	D	R	S	L	A	E	P	L	A	P	N	D	E	G	I	L	Y	A	D			
SEQIDNO:2-09751299	(217)	GQCYVLA	S	CATVS	-----	P	E	M	I	K	V	L	V	D	T	P	D	K	E	M	F	L	K	A	G	G	G	F	A	M	I	F	G	P	D	G	R	A	L	A	E	P	L	P	T	E	T	E	G	L	L	V	A	D
SEQIDNO:4-09751299	(214)	GQCFVLA	S	CALVS	-----	Q	S	M	I	D	M	L	C	T	D	D	E	K	H	A	L	L	L	A	G	G	G	H	S	R	I	I	G	P	D	G	D	L	V	A	P	L	A	E	N	E	E	G	I	L	Y	A	N	
Consensus (281)		GQCFVLA	A	Q	L	D	E	I	V	A	G	G	G	S	M	I	S	P	G	V	L	A	P	E	E	G	L	I	A	D																								

	(351)	351	360	370	380	390	400	410	420
gi_3228664_gb_AAC39136.1_	(262)	IDL SY VD TL RE MQPVFSHRRSDLYTLHINEKSSE--TGGL K FARFNIPADHIFYSTPHSFVFVNLKPVT D							
gi_3228670_gb_AAC39137.1_	(277)	VD LSV LQ SLYQTMPCFEHRRNDIYALTAYNLSKE P TQDRPFATNIVDKRTIFYESEHCFAFTNLR CV V K							
gi_3228666_gb_AAC39907.1_	(296)	ID LN YLR QL RR HL PV FQHRRPDLYGN L GHPLS----							
gi_3228668_gb_AAC40185.1_	(292)	ID L HF L Q Q MR QH L PV FQ HRRPDLYGS L GHPLS----							
gi_3242980_gb_AAC40184.1_	(292)	ID L HF L Q Q MR QH L PV FQ HRRPDLYGS L GHPLS----							
gi_2294001_emb_CAA02248.1_	(284)	ID LN QI Y GK W LL D PA GH YS TP GF LS L TFDQSEHV PV KK I GEQTNHFI S YEDLHEDKMDMLTIPPR RV AT							
gi_216934_dbj_BAA01994.1_	(280)	ID LS AIT L AK QA DP V GH Y SR PD VL SL N FNQRHT TP WN T A IST I H ATHTLV PQ SGALDGVRELNGADE QR							
gi_508735_gb_AAA19627.1_	(295)	LD LG D I AR AKLY FD V V GHY SK PD IF N L TVNEHPKK PV TF M TKVEKA ED SNK----							
gi_508733_gb_AAB60275.1_	(288)	LD LG D VAR AK LY FD S V GHY SR PD VL HL T VNEHPKK PV TF I SKVEKA ED SNK----							
gi_1469912_gb_AAB05220.1_	(288)	LD LG D VAR AK LY FD S V GHY SR PD VL HL T VNEHPKK PV TF I SKVEKA ED SNK----							
gi_1389699_gb_AAB05221.1_	(295)	ID LG D I AR AKLY FD S V GHY SR PD VL HL T VNEHPRK SV TF W TKVEKA ED SNK----							
gi_1181615_dbj_BAA11770.1_	(298)	LD LG E I AR AK FD D V V GH Y AR PE VL SL I VRDHAV SP VS FT STSSKA ES -SPK----							
gi_1171482_dbj_BAA09645.1_	(299)	LD LG E I AR AK FD D V V GH Y AR PE VL SL I VRDHAV SP VS FT STSSKA ES -SPK----							
gi_5953961_gb_AAE06465.1_	(280)	ID LS AIT L AK N PA DP V GHY SR PD VL RL G FNKAPQ PK V NI L G TEPSRT ST QC RPT TI RR SW RF PE-----							
SEQIDNO:2-09751299	(279)	ID LG M I AL AK AA AD PA GHY SR PD V TR LL L DR RP AQ R V VT L DA AF EPQ NED KGD AP AL RV VA ES AA AA Q--							
SEQIDNO:4-09751299	(276)	LD PG V RI L AK MA AD PA GHY SR PD I TR LL I DR SP KL P V VE I EG DL RP YAL G KAS ETGA QL EE I -----							
Consensus (351)		IDLG I AK D VGHYSRPDVL L V PV I							

Section 7

	(421)	421	430	440	450	460	470	480	490
gi_3228664_gb_AAC39136.1_	(330)	GHVLVSPKRVVPR	LTDLTDAETADLFI	VAKKVQAMLEKHH	NVTSTTICVQDGK	DAGQTVPHVHIHIL	PRR		
gi_3228670_gb_AAC39137.1_	(347)	GHVLVSTKRVT	PRLCGLDCAEMADM	FTTVCLVQRLLEKI	YQTTSATVTVQDGA	QAGQTVPHVHFHIM	PRR		
gi_3228666_gb_AAC39907.1_	(328)								
gi_3228668_gb_AAC40185.1_	(324)								
gi_3242980_gb_AAC40184.1_	(324)								
gi_2294001_emb_CAA02248.1_	(354)	A							
gi_216934_dbj_BAA01994.1_	(350)	ALPSTHSD	ETDRATASI						
gi_508735_gb_AAA19627.1_	(347)								
gi_508733_gb_AAB60275.1_	(340)								
gi_1469912_gb_AAB05220.1_	(340)								
gi_1389699_gb_AAB05221.1_	(347)								
gi_1181615_dbj_BAA11770.1_	(349)								
gi_1171482_dbj_BAA09645.1_	(350)								
gi_5953961_gb_AAE06465.1_	(345)								
SEQIDNO:2-09751299	(347)								
SEQIDNO:4-09751299	(338)								
Consensus (421)									

Section 8

	(491)	491	500	510	520	535
gi_3228664_gb_AAC39136.1_	(400)	AGDFG	DNEIYQK	LASHDK	EPERKPR	SRNEQMAEEAVVYRNLM---
gi_3228670_gb_AAC39137.1_	(417)	LGDFG	HNDQIYV	KLDERAE	-EKP	PRTIEERIEEAQIYRKFLTDIS
gi_3228666_gb_AAC39907.1_	(328)					
gi_3228668_gb_AAC40185.1_	(324)					
gi_3242980_gb_AAC40184.1_	(324)					
gi_2294001_emb_CAA02248.1_	(355)					
gi_216934_dbj_BAA01994.1_	(367)					
gi_508735_gb_AAA19627.1_	(347)					
gi_508733_gb_AAB60275.1_	(340)					
gi_1469912_gb_AAB05220.1_	(340)					
gi_1389699_gb_AAB05221.1_	(347)					
gi_1181615_dbj_BAA11770.1_	(349)					
gi_1171482_dbj_BAA09645.1_	(350)					
gi_5953961_gb_AAE06465.1_	(345)					
SEQIDNO:2-09751299	(347)					
SEQIDNO:4-09751299	(338)					
Consensus (491)						